SEQUENCE LISTING

<110> McGILL UNIVERSITY
       SZYF, Moshe
       BHATTACHARYA, Sanjoy K.
       RAMCHANDANI, Shyam

<120> DNA DEMETHYLASE, THERAPEUTIC AND
      DIAGNOSTIC USES THEREOF

<130> 1770-183"PCT" FC/ld

<150> CA 2,220,805
<151> 1997-11-12

<150> CA 2,230,991
<151> 1998-05-11

<160> 10

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 1804
<212> DNA
<213> Unknown

<220>
<223> cDNA encoding human demethylase

C_1

<400> 1

```
ccgctctgcg ggcggggcgg gtctccggga ttccaagggc tcggttacgg aagaagcgca       60
gagccggctg gggagggggc tggatgcgcg cgcacccggg gggaggccgc tgctgcccgg      120
agcaggagga gggggagagc gcggcggggcg gcagcggcgc tggcggcgac tccgccatag      180
agcagggggg ccagggcagc gcgctcgctc cgtccccggt gagcggcgtg cgcagggaag      240
gcgctcgggg cggcggccgt ggccggggggc ggtggaagca ggcggcccgg ggcggcggcg      300
tctgtggccg tggccgtggc cgtggccggg gtcggggccg tggccggggc cggggccggg      360
gccgcggccg tccccagagt ggcggcagcg gccttggcgg cgacggcggc ggcggcgcgg      420
gcggctgcgg cgtcggcagc ggtggcggcg tcgcccccccg gcgggatcct gtcccttttcc      480
cgtcggggag ctcggggccg gggcccaggg gaccccgggc cacggagagc gggaagagga      540
tggactgccc ggccctcccc cccggatgga agaaggagga agtgatccga aaatcagggc      600
tcagtgctgg caagagcgat gtctactact tcagtccaag tggtaagaag ttcagaagta      660
aacctcagct ggcaagatac ctgggaaatg ctgttgacct tagcagtttt gacttcagga      720
ccggcaagat gatgcctagt aaattacaga agaacaagca gagactccgg aatgaccccc      780
tcaatcagaa caagggtaaa ccagacctga acacaacatt gccaattaga caaactgcat      840
caattttcaa gcaaccagta accaaattca cgaaccaccc gagcaataag gtgaagtcag      900
accccccagcg gatgaatgaa caaccacgtc agcttttctg ggagaagagg ctacaaggac      960
ttagcgcatc agatgtaaca gaacaaatta taaaaaccat ggagctacct aaaggtcttc     1020
aaggagtcgg tccaggtagc aatgacgaga cccttctgtc tgctgtggcc agtgctttac     1080
acacaagctc tgcgcccatc acaggacaag tctctgctgc cgtggaaaag aaccctgctg     1140
tttggcttaa cacatctcaa cccctctgca aagctttcat tgttacagat gaagacatta     1200
ggaaacagga agagcgagtc caacaagtac gcaagaaact ggaggaggca ctgatggccg     1260
acatcctgtc ccgggctgcg gacacggagg aagtagacat tgacatggac agtggagatg     1320
aggcgtaaga atatgatcag gtaactttcg actgaccttc cccaagagca aattgctaga     1380
aacagaatta aaacatttcc actgggtttc gcctgtaaga aaaagtgtac ctgagcacat     1440
agctttttaa tagcactaac caatgccttt ttagatgtat ttttgatgta tatatctatt     1500
attccaaatg atgtttattt tgaatcctag gacttaaaat gagtctttta taatagcaag     1560
cagggcccctt ccggtgcagt gcagctttga ggccaggtgc agtctactgg aaaggtagca     1620
cttacgtgaa atatttgttt cccccacagt tttaatataa acagatcagg agtaccaaat     1680
```

```
aagtttccca attaaagatt attatacttc actgtatata aacagatttt tatactttat    1740
tgaaagaaga tacctgtaca ttcttccatc atcactgtaa agacaaataa atgactatat    1800
tcac                                                                 1804
```

<210> 2
<211> 411
<212> PRT
<213> Unknown

<220>
<223> predicted amino acid of human demethylase

<400> 2

```
Met Arg Ala His Pro Gly Gly Gly Arg Cys Cys Pro Glu Gln Glu Glu
1               5                   10                  15
Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile
            20                  25                  30
Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
        35                  40                  45
Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
    50                  55                  60
Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
65                  70                  75                  80
Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
                85                  90                  95
Pro Pro Ser Gly Gly Ser Gly Leu Gly Asp Gly Gly Gly Cys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
            115                 120                 125
Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
    130                 135                 140
Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
145                 150                 155                 160
Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
                165                 170                 175
Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
            180                 185                 190
Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
        195                 200                 205
Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
    210                 215                 220
Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
225                 230                 235                 240
Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
                245                 250                 255
Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
            260                 265                 270
Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
    275                 280                 285
Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
    290                 295                 300
Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
305                 310                 315                 320
Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
                325                 330                 335
Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
            340                 345                 350
Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
        355                 360                 365
Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
    370                 375                 380
```

Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
385   390   395   400
Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
                405   410

<210> 3
<211> 1589
<212> DNA
<213> Unknown

<220>
<223> cDNA sequence of human dMTase2

<400> 3
cacgcgcggg cgggtgggcg gagcggcccc cctagcgggg gctgtgaagc gcggggaggg   60
ggccgagcgg gtggcgaagc cggcgcgcgc ccggctgggg gcggagggcg gaggcccgtg   120
ggacagaaca gctgcggcga gtggcggcgg cggagggagc cgaatcggcg acgagcccgg   180
gggtcgcaac ttgcagaagc ggcggcggcg gcggcatcgg ccacggcggg cggaaaagcc   240
ggggcgcaat ggagcggaag aggtgggagt gcccggcgct cccgcagggc tgggaaaggg   300
aagaagtgcc caggaggtcg gggctgtcgg ccggccacag ggatgtcttt tactatagcc   360
ccagcgggaa gaagttccgc agcaagccac aactggcacg ttacctgggc ggatccatgg   420
acctcagcac cttcgacttc cgcaccggaa agatgttgat gaacaagatg aataagagtc   480
gccagcgtgt gcgctatgat tcttccaacc aggtcaaggg caagcctgac ctgaacaccg   540
cgctgcctgt acggcagact gcatccatct tcaagcaacc ggtgaccaag atcaccaacc   600
accccagcaa caaggtcaag agcgacccgc agaaggcagt ggaccagccg aggcagcttt   660
tctgggagaa gaagctaagt ggattgagtg cctttgacat tgcagaagaa ctggtcagga   720
ccatggactt gcccaagggc ctgcagggag tgggccctgg ctgtacagat gagacgctgc   780
tgtcagccat tgcgagtgct ctacacacca gcaccctgcc cattacaggc cagctctctg   840
cagccgtgga gaagaaccct ggtgtgtggc tgaacactgc acagccactg tgcaaagcct   900
tcatggtgac agatgacgac atcaggaagc aggaggagct ggtacagcag gtacggaagc   960
gcctggagga ggcactgatg ccgacatgc tagctcatgt ggaggagctt gcccgagacg   1020
gggaggcacc actggacaag gcctgtgcag aggaggaaga ggaggaggaa gaggaggagg   1080
aagagccgga gccagagcga gtgtagcaca ggtgccctgc caagtctgg gctgcagact   1140
gccttcagcc ttgcctggac caggtagggg ccagacctgt aggaggcagc cgtccacctc   1200
ctttccaaag cctcctgctt ccaggtctca gtgcagggag cccctgtgga ccttgaactc   1260
acttgtccct gcgctgcctg gcaggaagcc ccacactgaa agcagatgag cagtgaccca   1320
actgagaggc cacctggaca cagtcacctc cctgcctcct tatcatagga caaggccttg   1380
cttggcaccg aggagctggg agccgtgttg ggtgctggag gaagtttctg gaaacacacc   1440
tggctatgcc caccttatgt ccctaaggct attacaggcc agggtttgga ctgctccggc   1500
ccacagggct gcccagcctc cccacactga gggtcagcag cccaccagga agtcactttc   1560
cttcaataaa ctgatggtag gaacttgtg   1589

<210> 4
<211> 291
<212> PRT
<213> Unknown

<220>
<223> predicted amino acid sequence of human dMTase2

<400> 4
Met Glu Arg Lys Arg Trp Glu Cys Pro Ala Leu Pro Gln Gly Trp Glu
1   5   10   15
Arg Glu Glu Val Pro Arg Arg Ser Gly Leu Ser Ala Gly His Arg Asp
                20   25   30
Val Phe Tyr Tyr Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
            35   40   45
Leu Ala Arg Tyr Leu Gly Gly Ser Met Asp Leu Ser Thr Phe Asp Phe
        50   55   60
Arg Thr Gly Lys Met Leu Met Ser Lys Met Asn Lys Ser Arg Gln Arg
65   70   75   80

```
Val Arg Tyr Asp Ser Ser Asn Gln Val Lys Gly Lys Pro Asp Leu Asn
                85                  90              95
Thr Ala Leu Pro Val Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
            100              105             110
Thr Lys Ile Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
            115              120             125
Lys Ala Val Asp Gln Pro Arg Gln Leu Phe Trp Glu Lys Lys Leu Ser
        130              135             140
Gly Leu Asn Ala Phe Asp Ile Ala Glu Glu Leu Val Lys Thr Met Asp
145              150             155             160
Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Cys Thr Asp Glu Thr
                165             170             175
Leu Leu Ser Ala Ile Ala Ser Ala Leu His Thr Ser Thr Met Pro Ile
            180             185             190
Thr Gly Gln Leu Ser Ala Ala Val Glu Lys Asn Pro Gly Val Trp Leu
            195             200             205
Asn Thr Thr Gln Pro Leu Cys Lys Ala Phe Met Val Thr Asp Glu Asp
    210             215             220
Ile Arg Lys Gln Glu Glu Leu Val Gln Gln Val Arg Lys Arg Leu Glu
225             230             235             240
Glu Ala Leu Met Ala Asp Met Leu Ala His Val Glu Glu Leu Ala Arg
            245             250             255
Asp Gly Glu Ala Pro Leu Asp Lys Ala Cys Ala Glu Asp Asp Asp Glu
            260             265             270
Glu Asp Glu Glu Glu Glu Glu Glu Glu Pro Asp Pro Asp Pro Glu Met
    275             280             285
Glu His Val
290
```

```
<210> 5
<211> 1966
<212> DNA
<213> Unknown

<220>
<223> cDNA sequence of mouse dMTase1

<400> 5
gggggcgtgg cccccgagaag gcggagacaa gatggccgcc catagcgctt ggaggaccta    60
agaggcggtg gccggggcca cgccccgggc aggagggccg ctctgtgcgc gcccgctcta   120
tgatgcttgc gcgcgtcccc cgcgcgccgc gctgcgggcg gggcgggtct ccgggattcc   180
aagggctcgg ttacggaaga agcgcagcgc cggctgggga gggggctgga tgcgcgcgca   240
cccgggggga ggccgctgct gcccggagca ggaggagggg gagagtgcgg cgggcggcag   300
cggcgctggc ggcgactccg ccatagagca gggggggccag ggcagcgcgc tcgccccgtc   360
cccggtgagc ggcgtgcgca gggaaggcgc tcggggcggc ggccgtggcc ggggcggtg   420
gaagcaggcg ggccggggcg gcggcgtctg tggccgtggc cggggccggg gccgtggccg   480
gggacgggga cggggccggg gccggggccg cggccgtccc ccgagtggcg gcagcggcct   540
tggcggcgac ggcggcggct gcggcggcgg cggcagcggt ggcggcggcg cccccggcg   600
ggagccggtc cctttcccgt cggggagcgc ggggccgggg cccaggggac cccgggccac   660
ggagagcggg aagaggatgg attgcccggc cctcccccc ggatggaaga aggaggaagt   720
gatccgaaaa tctgggctaa gtgctggcaa gagcgatgtc tactacttca gtccaagtgg   780
taagaagttc agaagcaagc ctcagttggc aaggtacctg ggaaatactg ttgatctcag   840
cagttttgac ttcagaactg gaaagatgat gcctagtaaa ttacagaaga caaacagag   900
actgcgaaac gatcctctca atcaaaataa gggtaaacda gacttgaata caacattgcc   960
aattagacaa acagcatcaa ttttcaaaca accggtaacc aaagtcacaa atcatcctag  1020
taataaagtg aaatcagacc cacaacgaat gaatgaacag ccacgtcagc ttttctggga  1080
gaagaggcta caaggactta gtgcatcaga tgtaacagaa caaattataa aaaccatgga  1140
actacccaaa ggtcttcaag gagttggtcc aggtagcaat gatgagaccc ttttatctgc  1200
tgttgccagt gctttgcaca caagctctgc gccaatcaca gggcaagtct ccgctgctgt  1260
ggaaaagaac cctgctgttt ggcttaacac atctcaaccc ctctgcaaag ctttttattgt  1320
cacagatgaa gacatcagga aacaggaaga gcgagtacag caagtacgca agaaattgga  1380
```

```
agaagcactg atggcagaca tcttgtcgcg agctgctgat acagaagaga tggatattga    1440
aatggacagt ggagatgaag cctaagaata tgatcaggta actttcgacc gactttcccc    1500
aagrgaaaat tcctagaaat tgaacaaaaa tgtttccact ggcttttgcc tgtaagaaaa    1560
aaaatgtacc cgagcacata gagctttta atagcactaa ccaatgcctt tttagatgta    1620
ttttgatgt atatatctat tattcaaaaa atcatgttta ttttgagtcc taggacttaa    1680
aattagtctt ttgtaatatc aagcaggacc ctaagatgaa gctgagcttt tgatgccagg    1740
tgcaatctac tggaaatgta gcacttacgt aaaacatttg tttcccccac agttttaata    1800
agaacagatc aggaattcta aataaatttc ccagttaaag attattgtga cttcactgta    1860
tataaacata tttttatact ttattgaaag gggacacctg tacattcttc catcatcact    1920
gtaaagacaa ataaatgatt atattcacaa aaaaaaaaaa aaaaaa                   1966
```

<210> 6
<211> 414
<212> PRT
<213> Unknown

<220>
<223> predicted amino acid sequence of mouse dMTase1

<400> 6

```
Met Arg Ala His Pro Gly Gly Gly Arg Cys Cys Pro Glu Gln Glu Glu
1               5                   10                  15
Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile
            20                  25                  30
Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
        35                  40                  45
Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
    50                  55                  60
Lys Gln Ala Ala Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
65                  70                  75                  80
Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
                85                  90                  95
Pro Gln Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Gly Ala
            100                 105                 110
Gly Gly Cys Gly Val Gly Ser Gly Gly Gly Val Ala Pro Arg Arg Asp
            115                 120                 125
Pro Val Pro Phe Pro Ser Gly Ser Ser Gly Pro Gly Pro Arg Gly Pro
        130                 135                 140
Arg Ala Thr Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro
145                 150                 155                 160
Gly Trp Lys Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly
                165                 170                 175
Lys Ser Asp Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser
            180                 185                 190
Lys Pro Gln Leu Ala Arg Tyr Leu Gly Asn Ala Val Asp Leu Ser Ser
            195                 200                 205
Phe Asp Phe Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn
        210                 215                 220
Lys Gln Arg Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro
225                 230                 235                 240
Asp Leu Asn Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys
                245                 250                 255
Gln Pro Val Thr Lys Phe Thr Asn His Pro Ser Asn Lys Val Lys Ser
            260                 265                 270
Asp Pro Gln Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys
            275                 280                 285
Arg Leu Gln Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys
        290                 295                 300
Thr Met Glu Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn
305                 310                 315                 320
Asp Glu Thr Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser
```

```
                 325                      330                      335
  Ala Pro Ile Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala
                340                      345                      350
  Val Trp Leu Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr
            355                      360                      365
  Asp Glu Asp Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys
        370                      375                      380
  Lys Leu Glu Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp
  385                      390                      395                      400
  Thr Glu Glu Val Asp Ile Asp Met Asp Ser Gly Asp Glu Ala
                    405                      410
```

```
      <210>  7
      <211>  2392
      <212>  DNA
      <213>  Unknown

      <220>
      <223>  cDNA sequence of mouse dMTase2

      <400>  7
```

```
agcgggccga ggagccgggc gcaatggagc ggaagaggtg ggagtgcccg gcgctcccgc      60
agggctggga gagggaagaa gtgcccagaa ggtcggggct gtcggccggc cacagggatg     120
tcttttacta tagcccgagc gggaagaagt tccgcagcaa gccgcagctg gcgcgctacc     180
tgggcggctc catggacctg agcaccttcg acttccgcac gggcaagatg ctgatgagca     240
agatgaacaa gagccgccag cgcgtgcgct acgactcctc caaccaggtc aagggcaagc     300
ccgacctgaa cacggcgctg cccgtgcgcc agacggcgtc catcttcaag cagccggtga     360
ccaagattac caaccacccc agcaacaagg tcaagagcga cccgcagaag gcggtggacc     420
agccgcgcca gctcttctgg gagaagaagc tgagcggcct gaacgccttc gacattgctg     480
aggagctggt caagaccatg gacctcccca agggcctgca gggggtggga cctggctgca     540
cggatgagac gctgctgtcg gccatcgcca gcgccctgca cactagcacc atgcccatca     600
cgggacagct ctcggccgcc gtggagaaga accccggcgt atggctcaac accacgcagc     660
ccctgtgcaa agccttcatg gtgaccgacg aggacatcag gaagcaggaa gagctggtgc     720
agcaggtgcg gaagcggctg gaggaggcgc tgatggccga catgctggcg cacgtggagg     780
agctggcccg tgacggggag gcgccgctgg acaaggcctg cgctgaggac gacgacgagg     840
aagacgagga ggaggaggag gaggagcccg acccggaccc ggagatggag cacgtctagg     900
gcagaggccc tgccgagagc ccgtgctgcc tgctggagcc gcctgcagac gcggtcctcg     960
gccccacgtg aaccaggctc ggcggcgaag cccagccttg agacaccca ggaggaaggc     1020
cgtgctcctg ctccctcct cggcccgtcc ccacttcccg gggcctcggg cacacagct     1080
ggggctgccc ccacccgaaa gaccctccac gctcgtcctc tacagagtcc ggcttcggga     1140
agtgccgggt gctcctgggc cctgcctggc tccctacgac ctttgggctc gaggccagct     1200
cctccccatg cccgctgtcc cagctccttg agactggaga gcagccagca ggtgcccggc     1260
agctcggcgc cacggcttgc tgacagctgg gagggtttct cggtctggag gcgtagtttt     1320
gaaactcaca tcacccactg tgcagcgtga ggacgggact ctggtctgct gtggggggca     1380
tgcaggacgg cgccactctc tgccctgcca tgcggctggt ggtgccacag agcctcaccg     1440
tgcctgagtg gcgtgcccag ggaggccgct ctccttcagt aaatgtaaca cagtcgaggc     1500
acgtcatcgg gcagccttcc ctgtgtgcca acgccagcct tcgcttctga aaaccaaact     1560
ccagccgctg ccagtcggga cttggtcgcc cggcgctgcc agaatgctcc actgccagcc     1620
ggcccccctg cctcggtttc ccttctgttt agtggcgaca caggcaccca gctttggggt     1680
ggtgctgacg ctcccagggg tgccaggagc cactgggaca gggtgaggct cccagacgct     1740
cctcgaggtg cccagctctc cagggagctt ctggcccaag gcgttcttga gggatctgct     1800
ccttaacccc ccagtgcctt ggcgagggca ggttccaagc cacagacgcc tgccccgagt     1860
ggactttgcg gccagtccct gggtgccttc ctgggccctg cttgcccagt gagggttcct     1920
aacgggtggg ttcawtggcc tggcccvagc gagcccccac ctgcattgac cttaggccca     1980
tagagagggc ctgtcccggt gctgccccag ccaaggatct ggtcgctgcc cagggggac     2040
tgatgggcaa gagtcgcccc tgtggctgga ctgtgaccat ccctgatggg gcctgaccgc     2100
gggagctgag gaagcgccgc tccaccgtct gccctccaag acccgcatg gaggcagtgg     2160
gctggcagct tcctgctgct ccctgtcaga gtcaaagcac aaatcctcag acgggctca     2220
agggccaggg cagccgaggg aagctccagg tggggaccac gtcttcctga ggttggtgcc     2280
cactggctgg gaccctttgc agtggggtgg cctcccctct gtctgcctgg tggagggagc     2340
cgtgggcgtg gggacgtgac tgaataaagc caccatgggt ggatgtgctt gg             2392
```

<210> 8
<211> 285
<212> PRT
<213> Unknown

<220>
<223> predicted amino acid sequence of mouse dMTase2

<400> 8

```
Met Glu Arg Lys Arg Trp Glu Cys Pro Ala Leu Pro Gln Gly Trp Glu
1               5                   10                  15
Arg Glu Glu Val Pro Arg Arg Ser Gly Leu Ser Ala Gly His Arg Asp
            20                  25                  30
Val Phe Tyr Tyr Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
        35                  40                  45
Leu Ala Arg Tyr Leu Gly Gly Ser Met Asp Leu Ser Thr Phe Asp Phe
    50                  55                  60
Arg Thr Gly Lys Met Leu Met Asn Lys Met Asn Lys Ser Arg Gln Arg
65                  70                  75                  80
Val Arg Tyr Asp Ser Ser Asn Gln Val Lys Gly Lys Pro Asp Leu Asn
                85                  90                  95
Thr Ala Leu Pro Val Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
            100                 105                 110
Thr Lys Ile Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
        115                 120                 125
Lys Ala Val Asp Gln Pro Arg Gln Leu Phe Trp Glu Lys Lys Leu Ser
    130                 135                 140
Gly Leu Ser Ala Phe Asp Ile Ala Glu Glu Leu Val Arg Thr Met Asp
145                 150                 155                 160
Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Cys Thr Asp Glu Thr
                165                 170                 175
Leu Leu Ser Ala Ile Ala Ser Ala Leu His Thr Ser Thr Leu Pro Ile
            180                 185                 190
Thr Gly Gln Leu Ser Ala Ala Val Glu Lys Asn Pro Gly Val Trp Leu
            195                 200                 205
Asn Thr Ala Gln Pro Leu Cys Lys Ala Phe Met Val Thr Asp Asp Asp
    210                 215                 220
Ile Arg Lys Gln Glu Glu Leu Val Gln Gln Val Arg Lys Arg Leu Glu
225                 230                 235                 240
Glu Ala Leu Met Ala Asp Met Leu Ala His Val Glu Glu Leu Ala Arg
                245                 250                 255
Asp Gly Glu Ala Pro Leu Asp Lys Ala Cys Ala Glu Glu Glu Glu Glu
                260                 265                 270
Glu Glu Glu Glu Glu Glu Glu Pro Glu Pro Glu Arg Val
        275                 280                 285
```

<210> 9
<211> 17
<212> DNA
<213> Unknown

<220>
<223> sense primer for amplification of MBD domain
      of the putative demethylase candidate cDNA

<400> 9
ctggcaagag cgatgtc   17

<210> 10
<211> 22

<212> DNA
<213> Unknown

<220>
<223> antisense primer for amplification of MBD domain
of the putative demethylase candidate cDNA

<400> 10
agtctggttt acccttattt tg